国家自然科学奖

证　书

为表彰国家自然科学奖获得者，特颁发此证书。

项目名称：纤毛虫原生动物的分类学、发生与系统学以及生态学研究

奖励等级：二等

获 奖 者：徐奎栋（中国海洋大学）

中华人民共和国国务院

2005年1月8日

证书号：2004-Z-105-2-03-04

荣誉证书

授予徐奎栋同志：

第八届山东省青年科技奖

中共山东省委组织部　山东省人事厅　山东省科学技术协会

二〇〇八年五月

山东省人民政府

鲁政字〔2010〕70号

山东省人民政府
关于授予王伟等100名同志
山东省有突出贡献的中青年专家荣誉称号的通报

各市人民政府，各县（市、区）人民政府，省政府各部门、各直属机构，各大企业，各高等院校：

在省委、省政府的正确领导下，全省各级各部门认真学习贯彻《中共中央国务院关于进一步加强人才工作的决定》（中发〔2003〕16号）和《中共山东省委山东省人民政府关于实施人才强省战略进一步加强人才工作的意见》（鲁发〔2004〕10号），深入贯彻落实科学发展观，大力实施科教兴鲁、人才强省战略，努力推进“新世纪人才工程”建设，积极营造促进优秀人才脱颖而出的社会氛围，专业技术人才队伍建设不断取得新的成效，为

推动我省经济社会发展提供了强有力的人才和智力支持。全省广大专业技术人员认真履行岗位职责，刻苦钻研，扎实工作，勇于创新，无私奉献，涌现出一大批业绩突出、年富力强的中青年专家。根据《山东省有突出贡献的中青年专家选拔管理暂行办法》，经逐级推荐、选拔，评审委员会评审和公示、考察，省政府决定，授予王伟等100名同志“山东省有突出贡献的中青年专家”荣誉称号。

希望获得表彰的专家珍惜荣誉，再接再厉，取得更大成绩。各地、各部门、各单位要坚持以科学发展观为指导，切实把人才工作放在更加突出的位置，统筹抓好以高层次、创新型人才为重点的各类人才队伍建设，切实加强人才的培养、使用和管理、服务工作，进一步营造“尊重劳动、尊重知识、尊重人才、尊重创造”的良好社会氛围，为各类优秀人才脱颖而出、施展才干、建功立业创造条件。全省广大专业技术人员要以受表彰的专家为榜样，立足本职，拼搏创新，为建设经济文化强省，实现富民强省新跨越作出新的更大贡献。

附件：2009年度山东省有突出贡献的中青年专家名单

山东省人民政府

二〇一〇年四月一日

附件：

2009年度山东省有突出贡献的中青年专家名单

（共100名）

王　伟	济南二机床集团有限公司数控机床公司高级工程师
苏国海	济南市中心医院副院长兼心内科主任、主任医师
王吉万	青岛亨达集团有限公司技术中心主任、高级工程师
刘占杰	青岛海尔特种电气有限公司总经理、总工程师、工程技术应用研究员
张正欣	青岛饮料集团有限公司董事长、总经理、技术中心主任、高级工程师
郑生春	青岛市勘察测绘研究院副院长、工程技术应用研究员
张玉梅	淄博市竞技体育学校高级教练
高　志	滕州市中心人民医院呼吸科主任、主任医师
季俊昌	东营市教育科学研究院教科室副主任、中学高级教师
高振利	烟台毓璜顶医院泌尿外科主任、主任医师
翟延举	莱州市金海种业有限公司作物研究所所长

宋建波	山东南山铝业股份有限公司技术中心主任、高级工程师、高级经济师
唐文军	潍坊亚星化学股份有限公司总经理、高级工程师
邱栋	山东如意科技集团有限公司总裁、技术中心主任、工程技术应用研究员
王迎	泰安市泰山林业科学研究院副院长、研究员
张开利	山东泰山啤酒有限公司总工程师、工程技术应用研究员
戚建波	威海市第一中学副校长、中学一级教师
郑乾	三角集团有限公司工程子午胎技术处副处长、高级工程师
吕华	莱芜市植物保护站站长、农业技术推广研究员
车峰远	临沂市人民医院神经内科副主任、神经肌病科主任、副主任医师
王际海	德州市教学研究室副主任、中学高级教师
杨振峰	山东华鲁恒升化工股份有限公司技术中心主任、高级工程师
姜士宪	聊城市建设工程质量监督站工程技术应用研究员
李黎明	滨州职业学院副院长、教授
张国华	滨州渤海活塞股份有限公司副总经理、总工程师、研究员
林宪杰	菏泽学院院长助理、科研处处长、教授

马新	山东大学出版社总编辑、教授
吴臻	山东大学数学学院副院长、教授
孙康宁	山东大学材料科学与工程学院工程陶瓷实验室主任、教授
张彩明	山东大学计算机科学与技术学院应用技术研究所所长、教授
侯明	山东大学齐鲁医院肿瘤中心主任、主任医师
于良民	中国海洋大学海洋材料与防护技术教育部工程研究中心副主任、教授
杨桂朋	中国海洋大学化学化工学院院长、教授
刘永红	中国石油大学（华东）机电工程学院副院长、教授
葛际江	中国石油大学（华东）石油工程学院副教授
于衍真	济南大学土木建筑学院院长、教授
樊宝英	聊城大学文学院副院长、教授
刘焕阳	鲁东大学教务处处长、教授
刘均海	青岛大学物理科学学院教授
夏延致	青岛大学国家重点实验室培育基地副主任、教授
辛振祥	青岛科技大学高分子科学与工程学院院长、教授
武周虎	青岛理工大学环境学院教授
刘文锋	青岛理工大学土木工程学院教授
王富	青岛农业大学园林园艺学院副院长、教授
刘立山	曲阜师范大学数学学院院长、教授

张涛	山东财政学院教务处副处长、教授
范辉	山东工商学院计算机科学技术学院院长、教授
刘甦	山东建筑大学建筑城市规划学院院长、教授
刘培德	山东经济学院信息管理学院教授
时英	山东经济学院国际贸易学院院长、教授
尉永青	山东警察学院公共基础部副主任、教授
曾庆良	山东科技大学研究生教育学院院长、教授
孙宏飞	山东科技大学材料科学与工程学院教授
魏修亭	山东理工大学机械工程学院院长、教授
杜钦君	山东理工大学电气与电子工程学院教授
张民	山东农业大学资源与环境学院教授委员会主任、教授
杜金华	山东农业大学食品科学与工程学院教授
王瑞明	山东轻工业学院食品与生物工程学院院长、教授
刘素文	山东轻工业学院材料科学与工程学院教授
刘培玉	山东师范大学信息科学工程学院通信工程系主任、教授
唐汉卫	山东师范大学教育学院副院长、教授
魏平	山东体育学院体育社会科学系主任、教授
李庆忠	烟台大学化学生物理工学院应化所副所长、讲师
王修滋	大众报业集团经济导报社总编辑、高级编辑
王则才	肥城矿业集团有限责任公司副总工程师、工程技术

	应用研究员
王兴山	浪潮集团通用软件有限公司总经理、工程技术应用研究员
赵瑞东	山东超越数控电子有限公司总经理、技术总监、工程技术应用研究员
许洪强	山东电力集团公司调度中心主任、高级工程师
吕铭	莱芜钢铁股份有限公司炼钢厂厂长、高级工程师
李丰功	莱钢集团有限公司技术资源部副部长、工程技术应用研究员
孙柏	山东人民广播电台副台长、高级编辑
徐品	山东省地质环境监测总站副站长、研究员
朱永安	山东省淡水水产研究所副所长、研究员
杨合同	山东省科学院生物研究所所长、研究员
刘统玉	山东省科学院激光研究所副所长、研究员
李林光	山东省果树研究所研究室主任、研究员
王才斌	山东省花生研究所栽培室主任、研究员
曲辉英	山东省种子管理总站副站长、农业技术推广研究员
刘建军	山东省食品发酵工业研究设计院院长、研究员
刘爱华	山东福瑞达医药集团公司副总经理、主任药师
贾乃波	山东省水利勘测设计院院长、工程技术应用研究员
刘长余	山东省水利勘测设计院副院长、工程技术应用研究员

张文杰	山东省竞技体育学校、高级教练
赵跃然	山东省立医院、医学科学研究中心临床基础研究所副所长、研究员
王　欣	山东省立医院血液科主任、主任医师
陈宗波	青岛大学医学院附属医院儿科副主任、主任医师
杨传华	山东中医药大学附属医院院长、主任医师
王锡明	山东省医学影像学研究所CT室副主任、重点实验室主任、主任医师
王长生	山东石横特钢集团有限公司轧钢厂副厂长、技术中心副主任、工程技术应用研究员
邵　华	山东省职业卫生与职业病防治研究院副院长、研究员
王振平	兖矿集团有限公司通防部部长、工程技术应用研究员
王富奇	兖州煤业股份有限公司副总工程师、生产部部长、工程技术应用研究员
冀克俭	中国兵器工业集团第五三研究所第六研究室主任、研究员
高振会	国家海洋局北海环境监测中心主任、高级工程师（正高）
王增林	胜利石油管理局首席高级专家、高级工程师（正高）

杨耀忠	胜利石油管理局油田开发处副处长、高级工程师（正高）	
隋风贵	中石化胜利油田分公司地质科学研究院副院长、高级工程师（正高）	
徐奎栋	中国科学院海洋研究所海洋生物分类与系统演化实验室主任、研究员	✓
杨红生	中国科学院海洋研究所科研处处长、研究员	✓
孔　杰	中国水产科学研究院黄海水产研究所种质资源与工程育种实验室主任、研究员	

主题词：人事　表彰　通报

抄送：省委各部门，省人大常委会办公厅，省政协办公厅，省法院，省检察院，济南军区，省军区。
各民主党派省委。

山东省人民政府办公厅　　2010年4月2日印发

证　书

为表彰在促进海洋科学技术创新工作中做出突出贡献者，特颁发海洋科学技术奖证书，以资鼓励　。

证书编号：HKJ2012-G-2-A81-01

项目名称：海洋微型底栖生物调查规范制定及多样性研究

奖励等级：二等奖

获奖作者：徐奎栋【第1完成人】

奖励日期：二〇一三年五月三十一日

国家海洋局　　中国海洋学会

中国太平洋学会　　中国海洋湖沼学会

二〇一三年九月二日

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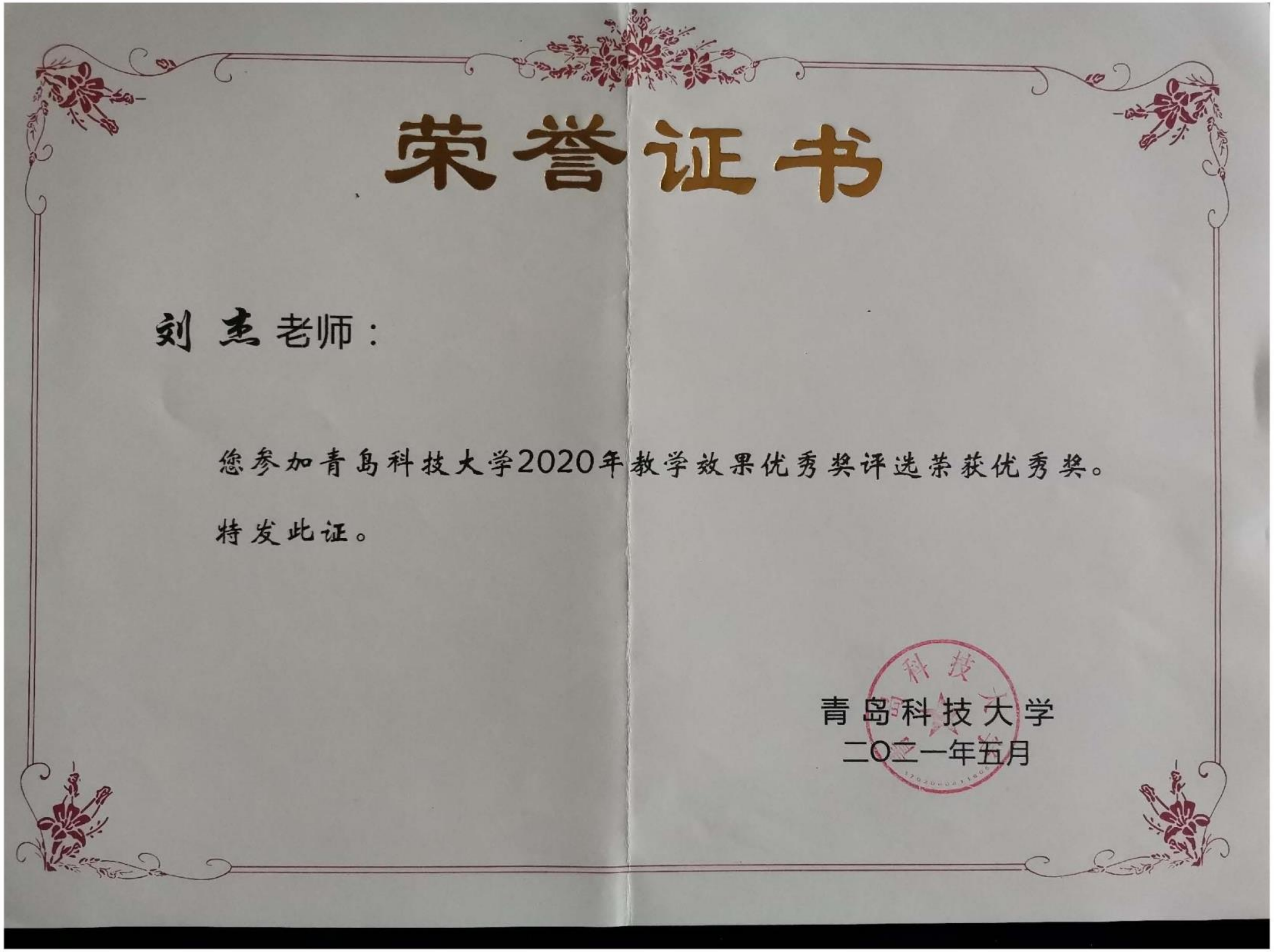

荣誉证书

刘杰老师：

您参加青岛科技大学2020年教学效果优秀奖评选荣获优秀奖。

特发此证。

青岛科技大学
二〇二一年五月

中国海洋工程咨询协会
China Association of Oceanic Engineering

为表彰在海洋经济社会发展和海洋科技进步中做出重要贡献的集体和个人，经中华人民共和国科学技术部核准登记，设立海洋工程科学技术奖（国科奖社字0221号）。

海洋工程科学技术奖

证书

项目名称： 海洋微生物资源采集与国家海洋微生物资源共享平台建设

奖励等级： 一等奖

获奖者： 刘杰

2013年1月11日

证书号：2012-01-03-G14

为表彰在促进科学技术进步工作中做出重大贡献，特颁发此证书。

获奖项目：17属豆科植物根瘤菌遗传多样性研究及7个根瘤菌新种的发表

获 奖 者：刘杰(第8完成人)

奖励等级：自然科学奖一等奖

奖励日期：2009年01月

证 书 号：2008-007

教育部

二〇〇九年一月二十日

山 东 省 教 育 厅

鲁教研函〔2019〕2号

山东省教育厅
关于公布2019年优秀博士学位论文优秀硕士学位论文和研究生优秀成果奖获奖名单的通知

各研究生培养单位:

根据《山东省学位委员会山东省教育厅山东省财政厅关于印发山东省研究生教育创新计划的通知》(鲁学位〔2006〕5号)要求，经单位推荐、专家评议和网上公示，2019年确定山东省优秀博士学位论文150篇，优秀硕士学位论文500篇，山东省研究生优秀成果奖500项，现将名单予以公布。

各单位要深入实施研究生教育创新计划，积极探索新形势下研究生教育规律，以培养研究生“创新意识、创造能力、创业精神”为核心，深化研究生培养模式改革，培养大批高层次专门人

才，为服务山东经济社会发展重大战略提供人才支持和智力支撑。

附件：1.2019年山东省优秀博士学位论文获奖名单
2.2019年山东省优秀硕士学位论文获奖名单
3.2019年山东省研究生优秀成果奖获奖名单

山东省教育厅
2019年12月27日

附件 2

2019年山东省优秀硕士学位论文获奖名单

（500篇）

序号	单位	姓名	论文题目	导师
1	山东大学	陈高进	7075 铝合金分流模挤压型材微观组织与力学性能研究	陈良
2	山东大学	陈晴	手指静脉识别中的形变问题研究	杨公平
3	山东大学	程海漫	危机学习的困境：基于学习过程论的分析	马奔
4	山东大学	迟长云	高活性钙基碳载体制备及其捕集 CO2 和脱除 HCl 研究	李英杰
5	山东大学	樊翠琴	IL-1β 介导的神经突触可塑性调节在抑郁症发病中的作用及机制	于书彦
6	山东大学	高桢	时间序列变化点检测算法研究及应用	卢国梁
7	山东大学	耿浩	中国金融行业宏观经济预测的同侪效应的结构模型估计	侯麟科
8	山东大学	管亚盟	形式解释论与实质解释论的立场之争与选择	刘军
9	山东大学	韩建平	固态电解质改性钛酸锂负极材料的制备及其电化学性能	白玉俊
10	山东大学	何文秀	氧化还原敏感的两亲性小分子药物递送系统的设计及体内外抗肿瘤评价	栾玉霞
11	山东大学	贾希彤	宏信息辅助的微表情识别研究	贲晛烨
12	山东大学	赖家辉	辣根过氧化物酶氧化对碘苯酚反应机理的理论研究	刘剑
13	山东大学	李彩军	同盟框架下泰国对美有限追随政策研究	杨鲁慧
14	山东大学	李明爽	裂纹自愈合陶瓷刀具的研制	黄传真
15	山东大学	刘命	重油富氧燃烧过程的 OH-PLIF 诊断实验研究	王志强

序号	单位	姓名	论文题目	导师
228	青岛科技大学	高越	基于夹点技术的环境风险管理方法	王芳
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RESEARCH ARTICLE

Comparative Genomics of *Exiguobacterium* Reveals What Makes a Cosmopolitan Bacterium

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ABSTRACT Although the strategies used by bacteria to adapt to specific environmental conditions are widely reported, fewer studies have addressed how microbes with a cosmopolitan distribution can survive in diverse ecosystems. *Exiguobacterium* is a versatile genus whose members are commonly found in various habitats. To better understand the mechanisms underlying the universality of *Exiguobacterium*, we collected 105 strains from diverse environments and performed large-scale metabolic and adaptive ability tests. We found that most *Exiguobacterium* members have the capacity to survive under wide ranges of temperature, salinity, and pH. According to phylogenetic and average nucleotide identity analyses, we identified 27 putative species and classified two genetic groups: groups I and II. Comparative genomic analysis revealed that the *Exiguobacterium* members utilize a variety of complex polysaccharides and proteins to support survival in diverse environments and also employ a number of chaperonins and transporters for this purpose. We observed that the group I species can be found in more diverse terrestrial environments and have a larger genome size than the group II species. Our analyses revealed that the expansion of transporter families drove genomic expansion in group I strains, and we identified 25 transporter families, many of which are involved in the transport of important substrates and resistance to environmental stresses and are enriched in group I strains. This study provides important insights into both the overall general genetic basis for the cosmopolitan distribution of a bacterial genus and the evolutionary and adaptive strategies of *Exiguobacterium*.

IMPORTANCE The wide distribution characteristics of *Exiguobacterium* make it a valuable model for studying the adaptive strategies of bacteria that can survive in multiple habitats. In this study, we reveal that members of the *Exiguobacterium* genus have a cosmopolitan distribution and share an extensive adaptability that enables them to survive in various environments. The capacities shared by *Exiguobacterium* members, such as their diverse means of polysaccharide utilization and environmental-stress resistance, provide an important basis for their cosmopolitan distribution. Furthermore, the selective expansion of transporter families has been a main driving force for genomic evolution in *Exiguobacterium*. Our findings improve our understanding of the adaptive and evolutionary mechanisms of cosmopolitan bacteria and the vital genomic traits that can facilitate niche adaptation.

KEYWORDS *Exiguobacterium*, cosmopolitan distribution, genomics, adaptation strategies, polysaccharide utilization, transporters

Across the landscape, microbial communities are nonrandomly dispersed in terms of their composition and diversity (1). Physical and chemical factors in the environment significantly influence the distribution patterns of microbes (2). For example,

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Bathymetric gradient shapes the community composition rather than the species richness of deep-sea benthic ciliates

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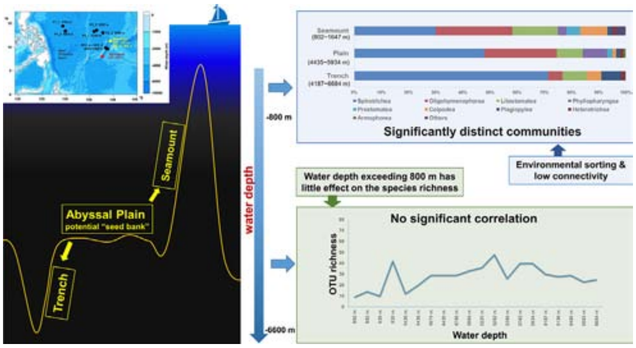
HIGHLIGHTS

- Benthic ciliate distribution across the deep-sea plain, seamount, and trench was investigated.
- Ciliate communities showed low connectivity along the bathymetric gradients.
- Most community dissimilarities were attributed to species replacement, caused by environmental sorting or historical constraints.
- Bathymetric gradient contributed more to community variations than geographic distance.

GRAPHICAL ABSTRACT



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ABSTRACT

The bathymetric gradient is one of the most important factors that regulate the distribution of life. However, community variations of benthic ciliates along bathymetric gradients in the deep sea remain rather unexplored. In this study, we hypothesize that in the deep sea, the bathymetric gradient shapes the benthic ciliate community composition rather than the species richness. Here, we evaluated the distribution patterns and drivers of benthic ciliate communities of an abyssal plain, a seamount, and a trench with water depths ranging from 800 m down to 6600 m by high throughput eDNA sequencing and statistical analyses. We observed no significant correlation between ciliate operated taxonomic unit (OTU) richness and water depth. A meta-analysis, which combined our previously published data from the neritic habitats, supports the notion that water depth exceeding 800 m has little effect on the richness of benthic ciliate species. In contrast, the composition of deep-sea ciliate communities was significantly distinct in different habitats along the bathymetric gradients. A SourceTracker analysis revealed extremely low connectivity among ciliate communities along the bathymetric gradients. More than 95% of the community dissimilarity in the deep-sea floor was attributed to species replacement, which might be caused by environmental sorting or historical constraints. Furthermore, the observed community variations could be ascribed more to water depth than to geographic distance. The findings imply that the strong force of environmental sorting along the bathymetric gradients and the low connectivity among the ciliate communities might lead to an isolated evolution. This could shape the community composition rather than the species richness, which is mainly determined by the limited nutrient availability and the extreme environmental conditions in the deep sea.

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Diversity and connectivity of microeukaryote communities across multiple habitats from intertidal zone to deep-sea floor in the Western Pacific Ocean

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Hydrothermal vent
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ABSTRACT

Habitat differentiation is the essential force for shaping animal and plant biogeography. Distribution patterns of microeukaryotes, which are an assemblage of highly diverse and phylogenetically distant groups, across multiple marine habitats remain largely unknown. We hypothesize that microeukaryote communities vary across different types of marine habitats at the regional scale similar as macroorganisms, and they are shaped by multiple factors. Herein, we evaluated the microeukaryotic diversity and connectivity in sediments from intertidal flat through continental shelf to deep-sea floor, including habitats of deep-sea plain, seamount, and hydrothermal vent, using high-throughput DNA sequencing. Microeukaryote communities were clustered into their own sub-groups according to the types of the habitats, where the communities of abundant taxa tended to gather with nearby habitats, while the rare taxa were mainly shaped by the types of the habitats. The SourceTracker analysis showed that the most probable sources for each community composition, particularly for those from seamounts and hydrothermal vent, were identified unknown. The continental shelf and deep-sea plain showed a relatively larger fraction of sources from each other, indicating a stronger source-sink dynamic than that among other habitats. The habitat differentiation contributed more to community variations than the spatial variables and water depth did. Co-occurrence network analysis indicated more complex bio-interactions in the neritic zone, where Cercozoa might play fundamental roles in the stability of the community than those in the deep sea, where ciliates were more connected with other taxa. Altogether, our findings highlight that the microeukaryotic communities are clearly shaped by the habitat differentiation, and this study also identifies the most probable source of dispersal for each community of different habitats.

1. Introduction

The knowledge of microbial biogeography directly influences our understanding on the global biodiversity and the underlying processes that shape their distribution (Bik et al., 2012). Revealing the patterns of microbial distribution along the space and environmental gradients is the major challenge in microbial ecology.

Microeukaryotes (= microbial eukaryotes) play a variety of critical roles in natural environments from primary producers, consumers, decomposers to parasites (Sherr et al., 2002; Caron et al., 2012; Edgcomb, 2016). Although they often comprise large standing stocks of biomass, it is difficult to observe them due to their small size and general absence of distinguishable morphological features (Lohan et al., 2017). The estimation of the diversity and distribution of microeukaryotes, particularly ciliates, has long been an ongoing debate and attracted considerable interests (Azovsky et al., 2020). Because of their high abundance, microbes are thought to be widespread or even cosmopolitan, and thus their diversity might be limited (Finlay, 2002). This hypothesis is supported by several studies based on morphological methods. For instance, no clear geographic clustering was found in marine benthic ciliates and flagellates, who are the major groups of microeukaryotes, based on the estimation of global diversity (Azovsky and Mazei, 2013; Azovsky et al., 2016). In contrast, Foissner (2008) proposed that the vast majority (>90%) of microeukaryotes are moderately or barely abundant, and

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Microeukaryote communities exhibit phyla-specific distance-decay patterns and an intimate link between seawater and sediment habitats in the Western Pacific Ocean

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ABSTRACT

Microeukaryotes are mainly composed of highly diverse and abundant protists, whose diversity and distribution in deep oceans have not been well studied. We investigated the vertical profiles of microeukaryotes throughout the water column down to abyssal sediments and their horizontal distribution over a distance of 1,300 km in the Western Pacific Ocean, using high throughput DNA sequencing. A distinct vertical distribution was detected for microeukaryote communities, which could be clustered into euphotic, aphotic and sediment groups. Nearly half of the operational taxonomic units detected in the sediment samples were also found in overlying water, indicating a frequent species exchange between seawater habitats and abyssal sediment habitats, which was similar to that observed for prokaryote communities. On the horizontal scaling side, a significant distance-decay relationship was found in the microeukaryote community. Furthermore, the major microeukaryotic groups revealed different distance-decay patterns which appeared to be significant for Dinoflagellata and Radiolaria, but insignificant for Ciliophora. Environmental selection contributed more to the variations in microeukaryote and Dinoflagellata communities than neutral processes, whereas neutral processes explained more variations in Radiolaria community. Generally, community variations explained by both processes were less than 30%, which was lower than that in coastal zones. These results imply that the complex distribution pattern within microeukaryote communities and more drivers, such as currents, water mass and biotic interactions, might contribute in shaping the distribution of microeukaryotes in the open ocean.

1. Introduction

Microeukaryotes (microbial eukaryotes) include the commonly-known algae, protozoa and lower fungi, and they are phylogenetically distant and highly diverse both in form and function. Because of their high diversity, their wide distribution and broad range of body sizes, protists, particularly ciliates, have triggered a debate regarding the diversity and distribution of microeukaryotes (Finlay, 2002; Foissner, 2008; Caron et al., 2012; Lentendu et al., 2018). This debate was mainly based on observations of freshwater and soil forms, as marine microeukaryotes have long been considered cosmopolitans (Hanson et al., 2012; Villarino, 2018). Recently, a growing number of studies has investigated the diversity and distribution of microeukaryotes in various marine habitats (de Vargas et al., 2015; Gimmler et al., 2016; Rocke et al., 2016; Filker et al., 2019). These studies revealed that communities of marine microeukaryotes generally exhibit a restricted distribution and a distance decay of community similarity, and they are strongly governed by environmental selection as well as neutral processes (dispersal-related), with varying relative importance in the coastal zone (e.g. Grattepanche et al., 2016; Wu et al., 2018; Zhang et al., 2018).

Among marine habitats, the deep ocean, though as the largest ecosystem, remains the least explored and understood (Ramirez-Llodra et al., 2010). Difficulties in the morphological identification of species and technical impediments have hampered the sampling, identification

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Baseline

Patterns and drivers of microeukaryotic distribution along the North Equatorial Current from the Central Pacific Ocean to the South China Sea

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ABSTRACT

Microeukaryotes have been recognized as highly abundant and diverse both in form and function, however, data on their diversity and distribution along marine currents remain scarce. Herein, the distribution of microeukaryotes in surface seawaters was analyzed along a 9000 km stretch of the North Equatorial Current (NEC) and its bifurcation using high throughput DNA sequencing. Significant distance-decay patterns were detected, and the microeukaryote communities were further divided into Central Pacific Ocean (CPO), Western Pacific Ocean (WPO), and South China Sea (SCS) groups. Statistical analyses suggested that the microeukaryotic assembly in the WPO is maintained by the CPO community transported via the NEC. Environmental selection contributed more to community variations than spatial processes did. Temperature and salinity were the two most important environmental factors to shape the examined communities. Altogether, characterizing the microeukaryotic diversity and distribution along the NEC provided an insight into the drivers of their distribution in open oceans.

Microeukaryotes, a highly abundant group of microorganisms, play various roles in natural environments, such as primary producers, predators, decomposers, and parasites (Sherr and Sherr, 2002; Caron et al., 2012; Edgcomb, 2016). They often comprise large standing stocks of biomass, yet their small size and indistinguishable general morphological features make them difficult to identify (Lohan et al., 2017). Subjects including the estimation of microeukaryote diversity and distribution have long attracted considerable interest and sparked ongoing debates (Finlay, 2002; Foissner et al., 2008; Caron et al., 2012; Lentendu et al., 2018; Moss et al., 2020).

Due to their small body size, high abundance and dormant life forms, microeukaryotes may have dispersal rates that surpass diversification, and thus have long been considered widespread or even cosmopolitan (Finlay, 2002; Hanson et al., 2012). Accordingly, microorganisms—such as microeukaryotes—should neither exhibit patterns of biogeography, nor display an increase in species richness from polar to equatorial regions, which is typical for some plants and animals (Moss et al., 2020). This theory is supported by studies on the global distribution of ciliates and flagellates based on morphological methods, which did not find clearly geographic clusters (Azovsky and Mazei, 2013; Azovsky et al., 2016). Furthermore, environmental factors related to latitude were suggested by Moss et al. (2020), which were thought to influence various macrofauna; such factors, however, may not define microbial diversity patterns of richness in the global ocean.

In contrast, recent molecular analytic methods have revealed an extremely high diversity of microorganisms, the rare taxa in particular (Pawlowski et al., 2011; Gimmler et al., 2016; Pernice et al., 2016; Filker et al., 2019; Wang et al., 2020). Distinct microeukaryotic distribution patterns were revealed in various marine habitats, i.e., subtropical harbors (Rocke et al., 2016), estuaries and coastlines (Filker et al., 2019), and deep-sea sediments (Pawlowski et al., 2011). These studies established that marine microeukaryote communities in isolated habitats and sediments commonly exhibit a distance-decay effect, and are strongly governed by environmental selection and neutral processes (e.

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